Phyre2

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Description	RVBD0909_(-)_1014685_1014864
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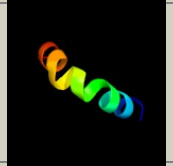
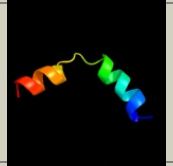
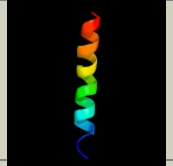
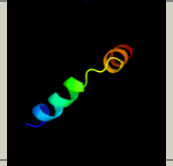
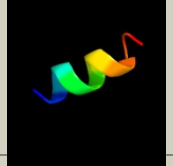
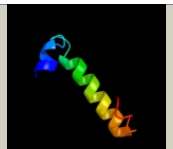
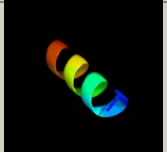
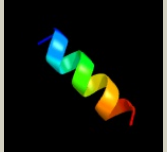
Unique Job ID	33263c134f36c49b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5uoiA_	Alignment		36.2	21	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**hhh_rd1_0142; **PDBTitle:** solution structure of the de novo mini protein hhh_rd1_0142
2	d1vmaa1	Alignment		23.3	25	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
3	c2jttD_	Alignment		22.3	29	**PDB header:**calcium binding protein/antitumor protei **Chain:** D: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of calcium loaded s100a6 bound to c-2 terminal siah-1 interacting protein
4	c1ezeA_	Alignment		19.1	39	**PDB header:**transferase inhibitor **Chain:** A: **PDB Molecule:**cholesteryl ester transferase inhibitor protein; **PDBTitle:** structural studies of a baboon (papio sp.) plasma protein2 inhibitor of cholesteryl ester transferase.
5	c2jttC_	Alignment		18.1	29	**PDB header:**calcium binding protein/antitumor protei **Chain:** C: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of calcium loaded s100a6 bound to c-2 terminal siah-1 interacting protein
6	c2jsaA_	Alignment		11.9	9	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**saposin-like protein family protein 5; **PDBTitle:** solution structure of caenopore-5 (81 pro trans confomer)
7	c1yycA_	Alignment		11.5	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative late embryogenesis abundant protein; **PDBTitle:** solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
8	c2g9lA_	Alignment		10.1	42	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**gaegurin-4; **PDBTitle:** the high-resolution solution conformation of an2 antimicrobial peptide gaegurin 4 and its mode of membrane3 interaction
9	c2o7hF_	Alignment		8.6	50	**PDB header:**transcription **Chain:** F: **PDB Molecule:**general control protein gcn4; **PDBTitle:** crystal structure of trimeric coiled coil gcn4 leucine zipper
10	d2cc6a1	Alignment		8.2	20	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
11	c5t76A_	Alignment		8.1	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**alanine--trna ligase, cytoplasmic; **PDBTitle:** a fragment of a human trna synthetase

12	c2vy8A_	Alignment		7.6	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** the 627-domain from influenza a virus polymerase pb22 subunit with glu-627
13	c1ij3C_	Alignment		7.4	43	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
14	c1ij3B_	Alignment		7.4	43	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
15	c3onrl_	Alignment		7.3	19	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
16	c1ij2C_	Alignment		7.2	43	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
17	c1swiA_	Alignment		7.2	43	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with benzene
18	c3k7zB_	Alignment		7.2	43	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
19	c1rb1A_	Alignment		7.2	43	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
20	c3k7zA_	Alignment		7.2	43	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
21	c1rb6C_	Alignment	not modelled	7.2	43	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
22	c1rb1B_	Alignment	not modelled	7.2	43	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
23	d1ryka_	Alignment	not modelled	6.8	15	**Fold:**SAM domain-like **Superfamily:**Hypothetical protein YjbJ **Family:**Hypothetical protein YjbJ
24	c1ij2B_	Alignment	not modelled	6.8	43	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
25	c2mqkA_	Alignment	not modelled	6.7	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent target dna activator b; **PDBTitle:** solution structure of n terminal domain of the mub aaa+ atpase
26	d2yrka1	Alignment	not modelled	6.5	12	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
27	c2vxaL_	Alignment	not modelled	6.2	31	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
28	d2g7ja1	Alignment	not modelled	5.9	43	**Fold:**Secretion chaperone-like **Superfamily:**YgaC/TfoX-N like **Family:**YgaC-like
						PDB header:apolipoprotein

29	c1iojA_	Alignment	not modelled	5.3	33	**Chain:** A: **PDB Molecule:**apoc-i; **PDBTitle:** human apolipoprotein c-i, nmr, 18 structures
30	c1ld4E_	Alignment	not modelled	5.3	58	**PDB header:**virus **Chain:** E: **PDB Molecule:**general control protein gcn4; **PDBTitle:** placement of the structural proteins in sindbis virus